Figure 1

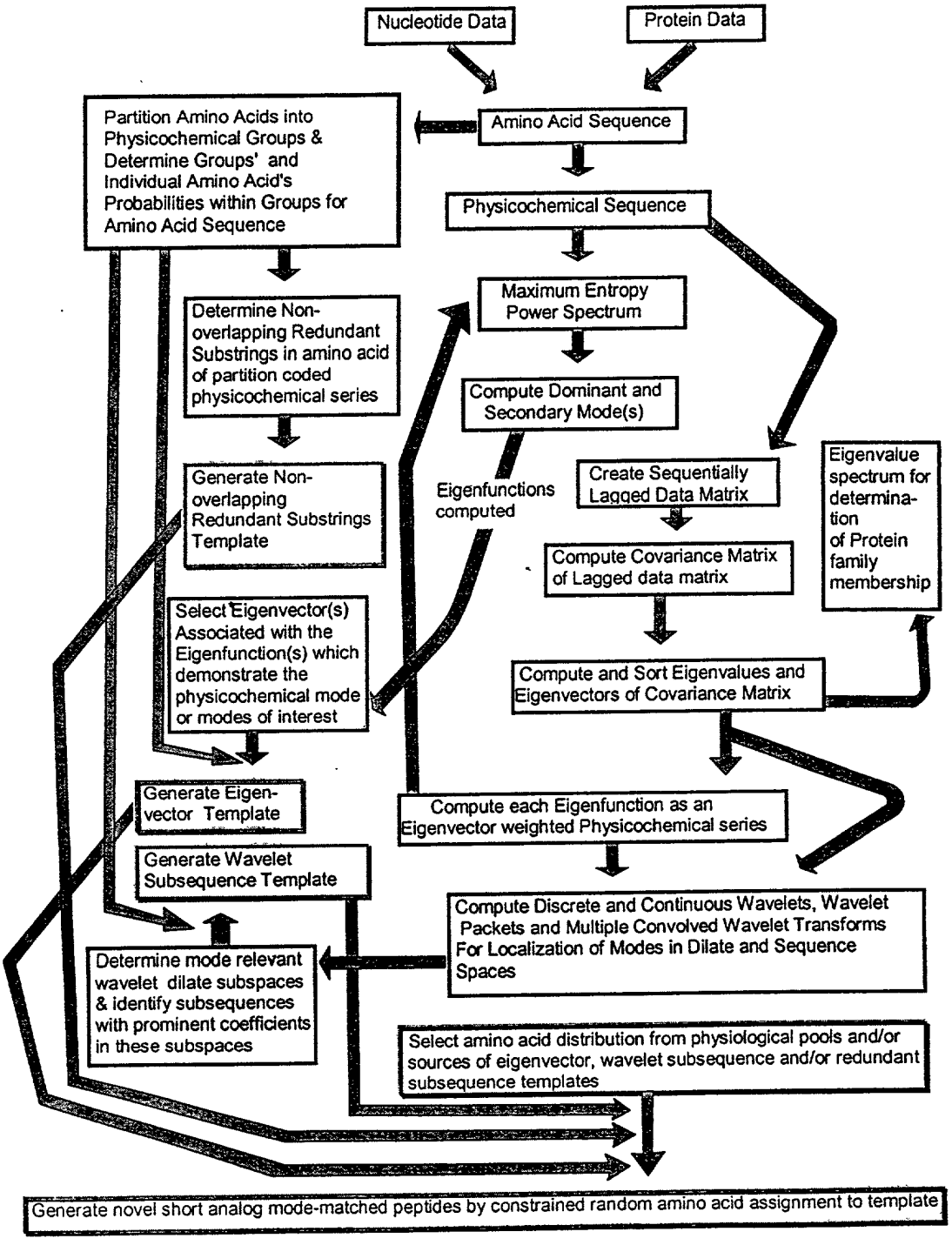

Nucleotide Data
Protein Data
Amino Acid Sequence
Partition Amino Acids into Physicochemical Groups & Determine Groups' and Individual Amino Acid's Probabilities within Groups for Amino Acid Sequence
Physicochemical Sequence
Maximum Entropy Power Spectrum
Determine Non-overlapping Redundant Substrings in amino acid of partition coded physicochemical series
Compute Dominant and Secondary Mode(s)
Generate Non-overlapping Redundant Substrings Template
Eigenfunctions computed
Create Sequentially Lagged Data Matrix
Eigenvalue spectrum for determination of Protein family membership
Compute Covariance Matrix of Lagged data matrix
Select Eigenvector(s) Associated with the Eigenfunction(s) which demonstrate the physicochemical mode or modes of interest
Compute and Sort Eigenvalues and Eigenvectors of Covariance Matrix
Generate Eigen-vector Template
Compute each Eigenfunction as an Eigenvector weighted Physicochemical series
Generate Wavelet Subsequence Template
Compute Discrete and Continuous Wavelets, Wavelet Packets and Multiple Convolved Wavelet Transforms For Localization of Modes in Dilate and Sequence Spaces
Determine mode relevant wavelet dilate subspaces & identify subsequences with prominent coefficients in these subspaces
Select amino acid distribution from physiological pools and/or sources of eigenvector, wavelet subsequence and/or redundant subsequence templates
Generate novel short analog mode-matched peptides by constrained random amino acid assignment to template

Figure 2

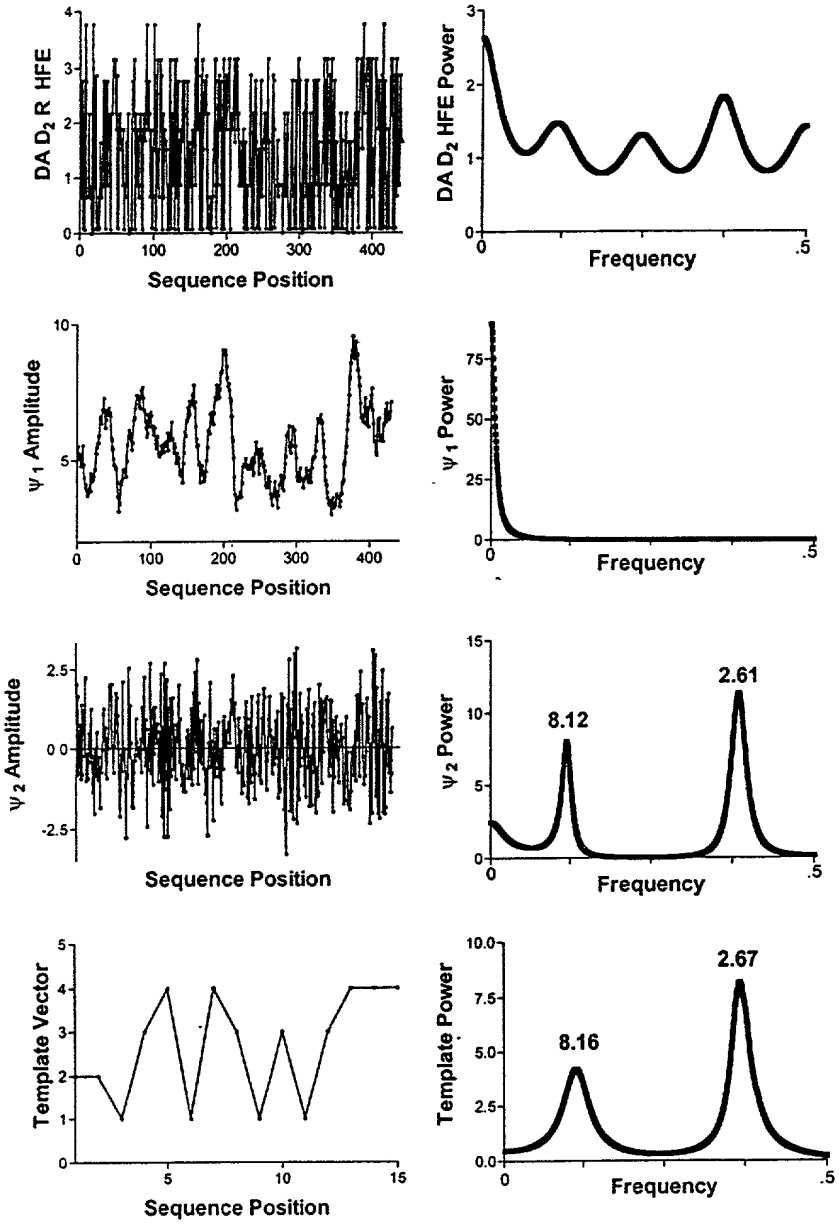

DA D2 R HFE
Sequence Position
DA D2 HFE Power
Frequency
ψ1 Amplitude
Sequence Position
ψ1 Power
Frequency
ψ2 Amplitude
Sequence Position
ψ2 Power
8.12
2.61
Frequency
Template Vector
Sequence Position
Template Power
8.16
2.67
Frequency

Fig. 3A

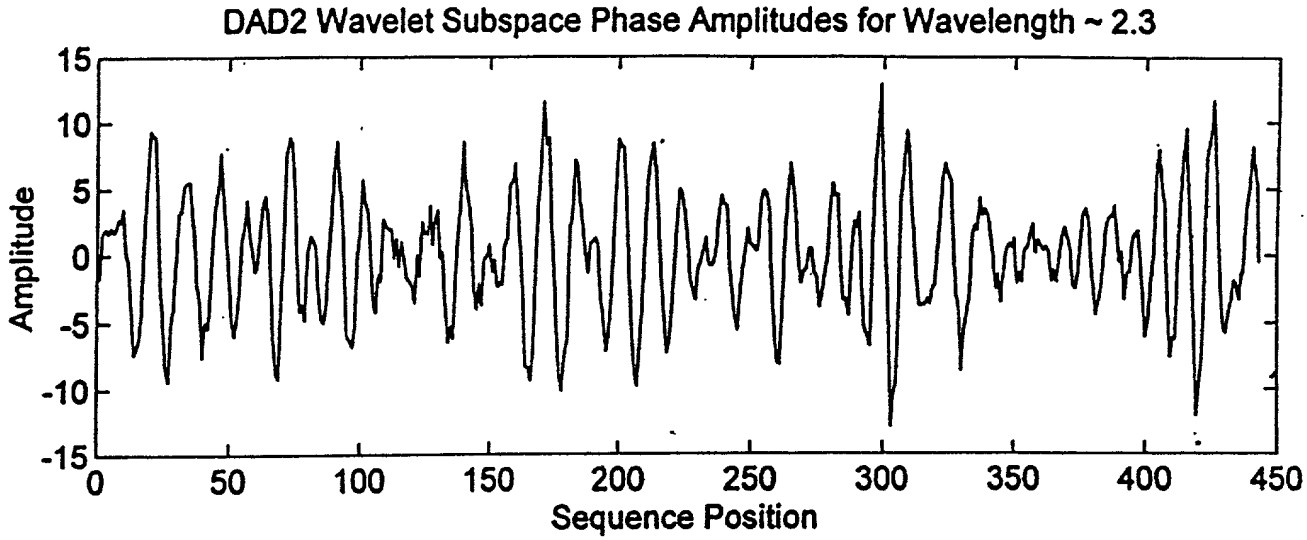

DAD2 Wavelet Subspace Phase Amplitudes for Wavelength ~ 2.3
Amplitude
Sequence Position
15
10
5
0
-5
-10
-15
0
50
100
150
200
250
300
350
400
450

Fig. 3B

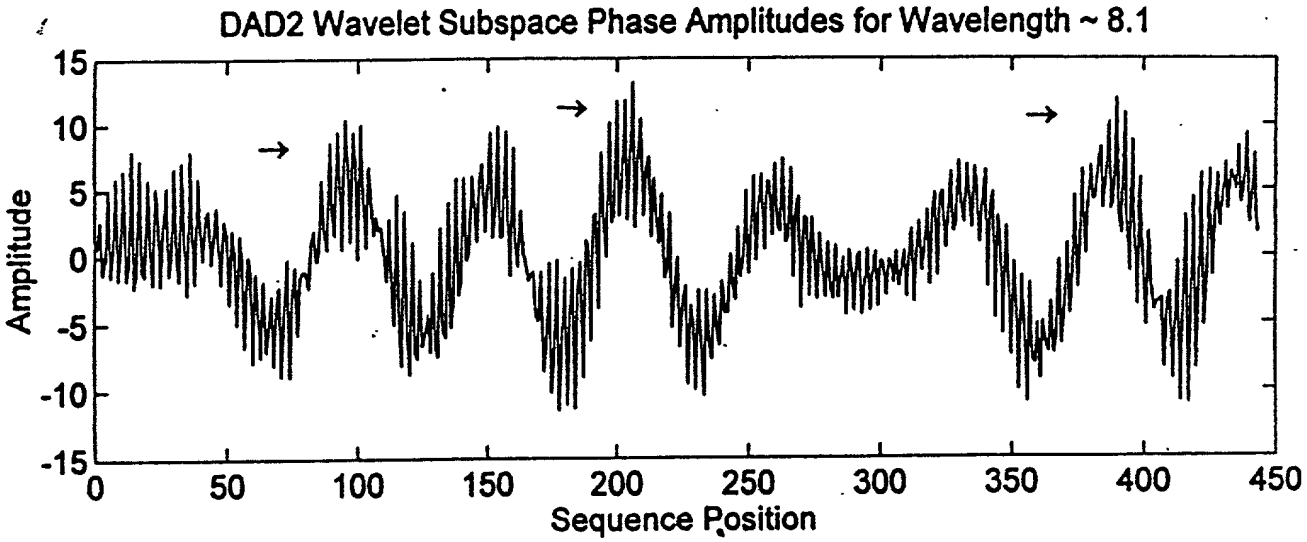

DAD2 Wavelet Subspace Phase Amplitudes for Wavelength ~ 8.1
Amplitude
Sequence Position
15
10
5
0
-5
-10
-15
0
50
100
150
200
250
300
350
400
450

Fig. 4A

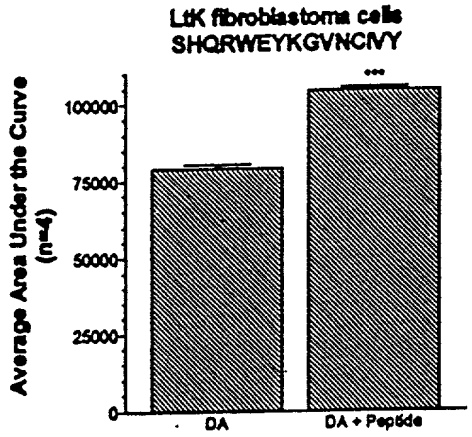


Fig. 4B

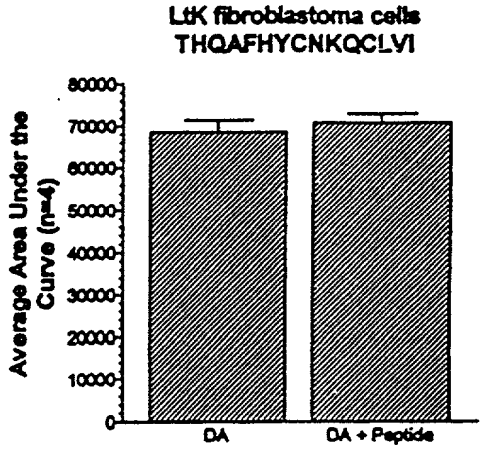


Fig. 4C

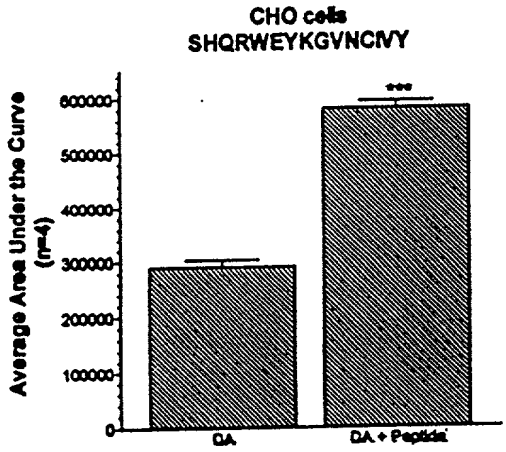


Fig. 4D

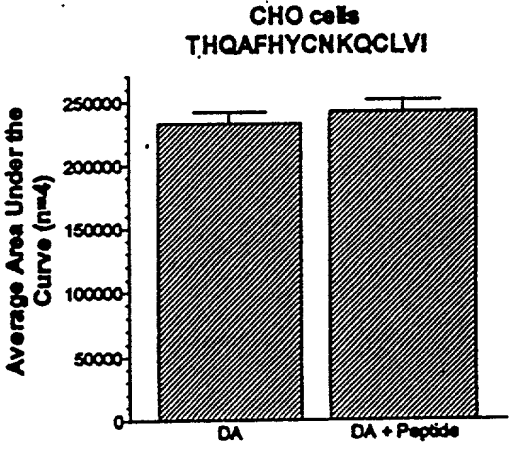


Fig. 5A

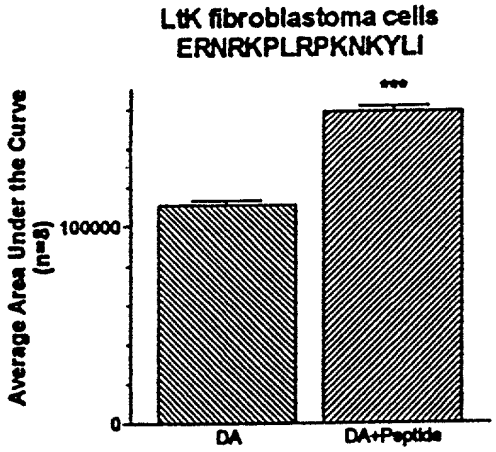


Fig. 5B

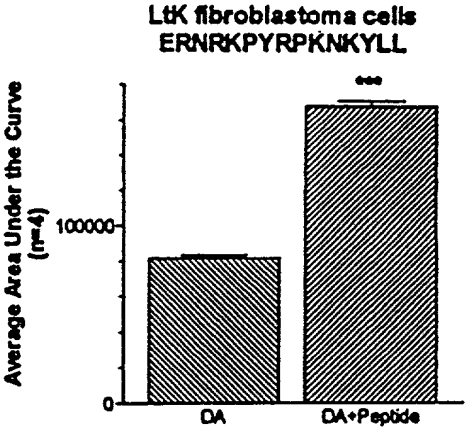


Fig. 5C

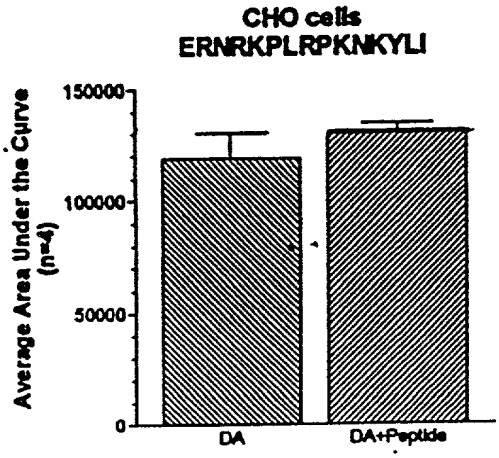


Fig. 5D

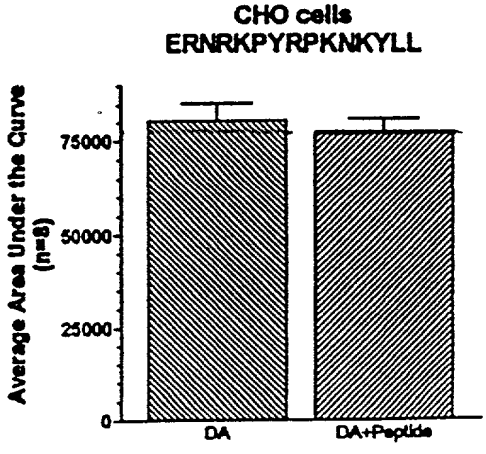
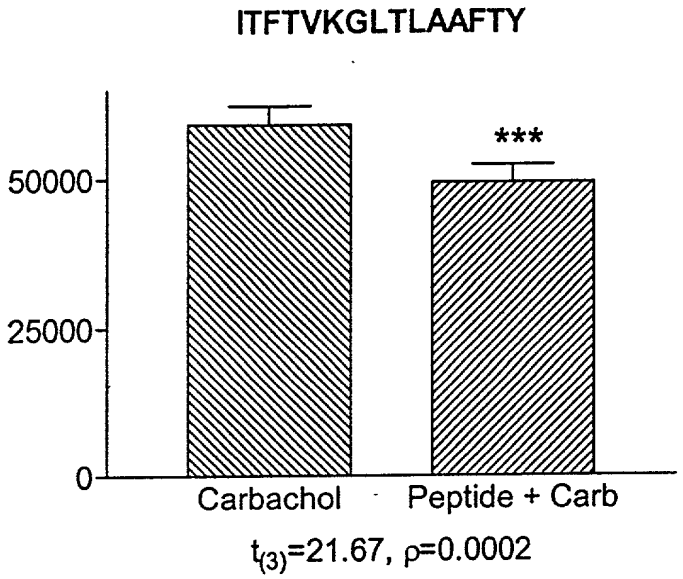
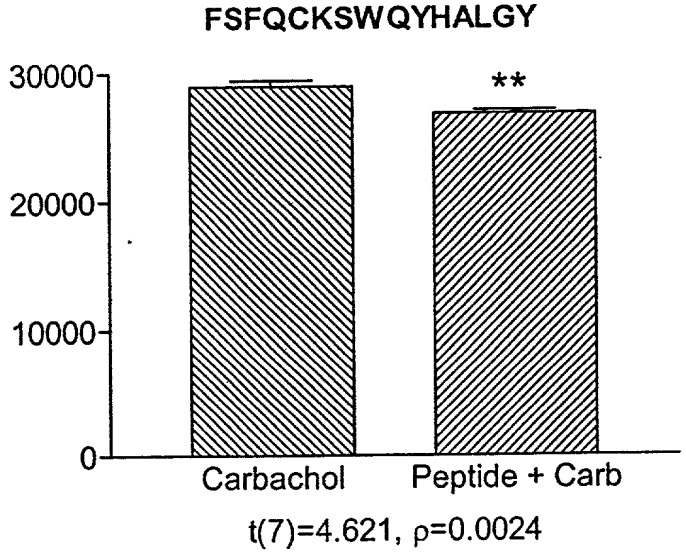


Figure 6

A


ITFTVKGLTLAAFTY
***
50000
25000
0
Carbachol
Peptide + Carb
$t_{(3)}$=21.67, ρ=0.0002

B


FSFQCKSWQYHALGY
**
30000
20000
10000
0
Carbachol
Peptide + Carb
t(7)=4.621, ρ=0.0024